



21581-265.seq.V3.ST25
SEQUENCE LISTING

<110> Kaneka Corporation
Matsuda, Hideyuki
Kawamukai, Makoto
Yajima, Kazuyoshi
Ikenaka, Yasuhiro
Hasegawa, Junzo
Takahashi, Satomi

<120> Process For Producing Coenzyme Q10

<130> 21581-00265-US

<140> 09/830,111

<141> 2001-07-23

<160> 9

<170> PatentIn version 3.2

<210> 1

<211> 1653

<212> DNA

<213> Saioella complicata

<400> 1

```
ttttgtgggg tcgaaaagtc ggcacgggtg caggttcggc ttgagaccag taaaggctcg      60
gagattgagt tcaggacaaa gctttgatcc gtgaggctca catcttcagc aaatcatttc      120
aaatccatat accatggcct caccagcact gcggatacga agcatcagct ctcgatcaat      180
cgcctctctg cgatecggta ccctaagaac agcctcggca ctttcattac gactaagatg      240
taccgacg agccggccat cgagttcatg ggctgctgct gtgtcttcgg cgtcgagact      300
ggttgagcct gatccgaatc aacctctcat caatccgctc aacttggtcg gtcccagat      360
gtcaaattctt acatccaaca tccgatctct cctcggttca ggacaccctt ctctcgacac      420
tgtcgctaaa tactatgttc agtctgaggg aaagcatatt cgtccgctca tgggtactgct      480
gatggctcag gcgacggagg ttgcgcaaaa agttcagggt tgggagaagg tcgtggagg      540
tccggtgaac gagggactcg caccaccaga ggtgctcaat gacaagaacc cagatatgat      600
gaacatgagg tcaggacat taacgaagga cggcgagatc gagggacaga cgtcgaatat      660
cctcgctcg caacggcggg tggctgagat cacggagatg atccatgcag catcactcct      720
ccacgacgac gttatcgacg cttccgagac cagacgaaac gcaccatccg gaaaccaggc      780
attcggaac aagatggcga ttttggtggt tgatttcttg ttgggacggg cgtctgttgc      840
attggcgagg ttgcgcaatc cggaggatg tgagcttttg gctactgtta ttgcaaactt      900
ggttgagggg gagttcatgc agttgaaaaa tactgttgat gatgcgattg aggctacggc      960
gacgcaggaa acgttcgatt actatttgca gaagacttac ttgaagactg cgtccttgat     1020
tgccaagtcg tgcagagcaa gtgcgcttct ggggtggtgct acgcctgagg ttgctgatgc     1080
```

21581-265.seq.V3.ST25

tgcttatgct tacggaagga accttggttt ggcatccag atcgctgacg acatgctcga 1140
 ctacaccgtc tccgctaccg acctcggtaa gcccgcgggt gcagacctcc agctcgggtct 1200
 cgccaccgcg ccggccctct tcgcatggaa gcaccacgcc gagctcggtc ccatgatcaa 1260
 gcgcaagttc tctgaccag gagacgtcga gcgtgcacgc gagttggtcg agaaaagtga 1320
 tggattggag aagacgagag ccttggcgga ggagtatgcc cagaaggcgt tggatgcaat 1380
 tcggacgttc ccggagagtc cggcacggaa ggctttggag cagttgacgg acaaggtggt 1440
 gactaggtca agataggaat tcgagctcgg taccgggga tcctctagag tcgacctgca 1500
 ggcattgcaag cttggctggt ttggcggatg agagaagatt ttcagcctga tacagattaa 1560
 atcagaacgc agaagcggtc tgataaaaca gaatttgctt ggcggcagta gcgcggtggt 1620
 cccacctgac cccatgccga actcagaagt gaa 1653

<210> 2
 <211> 446
 <212> PRT
 <213> Saitoella complicata

<400> 2

Ser Glu Gln Ile Asp Asn Met Ala Ser Pro Ala Leu Arg Ile Arg Ser
 1 5 10 15

Ile Ser Ser Arg Ser Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr
 20 25 30

Ala Ser Ala Pro Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro
 35 40 45

Ser Ser Ser Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu
 50 55 60

Pro Asp Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro
 65 70 75 80

Glu Met Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly
 85 90 95

His Pro Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu Gly
 100 105 110

Lys His Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala Thr Glu
 115 120 125

Val Ala Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu Val Pro Val
 130 135 140

21581-265.seq.V3.ST25

Asn Glu Gly Leu Ala Pro Pro Glu Val Leu Asn Asp Lys Asn Pro Asp
 145 150 155 160
 Met Met Asn Met Arg Ser Gly Pro Leu Thr Lys Asp Gly Glu Ile Glu
 165 170 175
 Gly Gln Thr Ser Asn Ile Leu Ala Ser Gln Arg Arg Leu Ala Glu Ile
 180 185 190
 Thr Glu Met Ile His Ala Ala Ser Leu Leu His Asp Asp Val Ile Asp
 195 200 205
 Ala Ser Glu Thr Arg Arg Asn Ala Pro Ser Gly Asn Gln Ala Phe Gly
 210 215 220
 Asn Lys Met Ala Ile Leu Ala Gly Asp Phe Leu Leu Gly Arg Ala Ser
 225 230 235 240
 Val Ala Leu Ala Arg Leu Arg Asn Pro Glu Val Ile Glu Leu Leu Ala
 245 250 255
 Thr Val Ile Ala Asn Leu Val Glu Gly Glu Phe Met Gln Leu Lys Asn
 260 265 270
 Thr Val Asp Asp Ala Ile Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp
 275 280 285
 Tyr Tyr Leu Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys
 290 295 300
 Ser Cys Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala
 305 310 315 320
 Asp Ala Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile
 325 330 335
 Val Asp Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly Lys
 340 345 350
 Pro Ala Gly Ala Asp Leu Gln Leu Gly Leu Ala Thr Ala Pro Ala Leu
 355 360 365
 Phe Ala Trp Lys His His Ala Glu Leu Gly Pro Met Ile Lys Arg Lys
 370 375 380
 Phe Ser Asp Pro Gly Asp Val Glu Arg Ala Arg Glu Leu Val Glu Lys
 385 390 395 400

21581-265.seq.V3.ST25

Ser Asp Gly Leu Glu Lys Thr Arg Ala Leu Ala Glu Glu Tyr Ala Gln
 405 410 415

Lys Ala Leu Asp Ala Ile Arg Thr Phe Pro Glu Ser Pro Ala Arg Lys
 420 425 430

Ala Leu Glu Gln Leu Thr Asp Lys Val Leu Thr Arg Ser Arg
 435 440 445

<210> 3
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer DPS-1

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> n stands for g, a, t, or c

<220>
 <221> misc_feature
 <222> (13)..(13)
 <223> n stands for g, a, t, or c

<400> 3
 aaggatcctn ytncaygayg aygt

24

<210> 4
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer DPS-1 1AS

<220>
 <221> misc_feature
 <222> (6)..(6)
 <223> n stands for g, a, t, or c

<220>
 <221> misc_feature
 <222> (15)..(15)
 <223> n stands for g, a, t, or c

<400> 4
 aryptgnadra aytcncc

17

<210> 5
 <211> 21
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primer Sa-1S

<400> 5

gagaccagac gaaacgcacc a

21

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer Sa-2AS

<400> 6

tggtgcgttt cgtctggtct c

21

<210> 7

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer Sa-N1

<400> 7

aacatatggc ctcaccagca ctgcgg

26

<210> 8

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer Sa-C

<400> 8

aagaattcct atcttgacct agtcaacac

29

<210> 9

<211> 8

<212> PRT

<213> Saitoella complicata

<400> 9

Gly Asp Phe Leu Leu Gly Arg Ala

1

5